

S4 Tolerance and adaptation to abiotic stresses

P18 Comparative structural analysis of the drought responsive dehydrin and aquaporin gene families in *Brachypodium* and close grasses

Sergio Gálvez Rojas¹, Federico Agostini², María Ángeles Decena³, Rosa Mérida García⁴, Pilar Catalán³, Pilar Hernández Molina⁴

1) ETSI Informática, Universidad de Málaga. Málaga, Spain 2) Instituto de Botánica del Nordeste, UNNE. Corrientes, Argentina

3) Escuela Politécnica Superior de Huesca, Universidad de Zaragoza. Huesca, Spain 4) Instituto de Agricultura Sostenible, CSIC. Córdoba, Spain

Dehydrins (DHNs) belong to the group 2 LEA (Late Embryogenesis Abundant) genes and play an important role in the response of plants to abiotic stress, mainly heat, salinity and drought. Under these stresses, DHNs accumulate to a large extent in maturing seeds and in all vegetative tissues. As many studies reveal, there is a positive correlation between DHN gene expression (synthesis of DHN proteins) and plant stress tolerance. Aquaporins (AQPs) belong to the major intrinsic protein (MIP) superfamily of membrane proteins conserved in plants and animals as well as in bacteria. Supporting evidence suggests that AQPs have an important role in stomatal closure and circadian regulation. There are more than 150 MIPs identified and, although some of them are constitutively expressed, others are regulated in response to drought and salinity.

In this study, sequence and annotation data has been retrieved from Phytozome and Ensembl Plants in order to compare DHNs and AQPs in four *Brachypodium* species, 54 *B. distachyon* varieties and five cereals (*Zea mays*, *Sorghum bicolor*, *Oryza sativa*, *Hordeum vulgare* and *Triticum aestivum*).

In the *B. distachyon* intra-species comparison, drought tolerant lines seem to contain slightly shorter aquaporin and dehydrin genes, and some of them are dissimilar to those of the rest. The physical distribution of AQPs includes a cluster of genes that splits the lines into two main groups depending on its location, either in chromosome 3 or in chromosome 4 of this species. However, this does not seem to be related to drought stress susceptibility.

A phylogenetic analysis of the dehydrin gene family shows a close relation between the *B. stacei* and *B. hybridum* - S subgenomes, followed by the *B. distachyon* and *B. hybridum* -D subgenome, and *B. sylvaticum*. However *B. sylvaticum*, typical from humid environments, contains nine DHNs, four of which are not close to any of the nine DHNs present in the other Mediterranean *Brachypodium* species. A deeper analysis of orthologs shows that a DHN in *B. distachyon* chromosome 1 is not related to those of *Sorghum* or *Oryza* and that there are clusters of DHNs in chromosomes 5 and 6 of *Triticum aestivum* related to those of chromosomes 3 and 4 of *B. distachyon*. Only one DHN in *Brachypodium* spp is found in all the analyzed grass species with the exception of *Hordeum vulgare*.

References:

Plant Signal Behav. 2011 Oct; 6(10): 1503–1509.

Biochim Biophys Acta. 2000 May 1;1465(1-2):324-42.

Physiol Rev. 2015 Oct;95(4):1321-58.

Funct Integr Genomics. 2019 Mar;19(2):295-309.